

FIG. 1

GENETICALLY ENGINEERED VACCINE

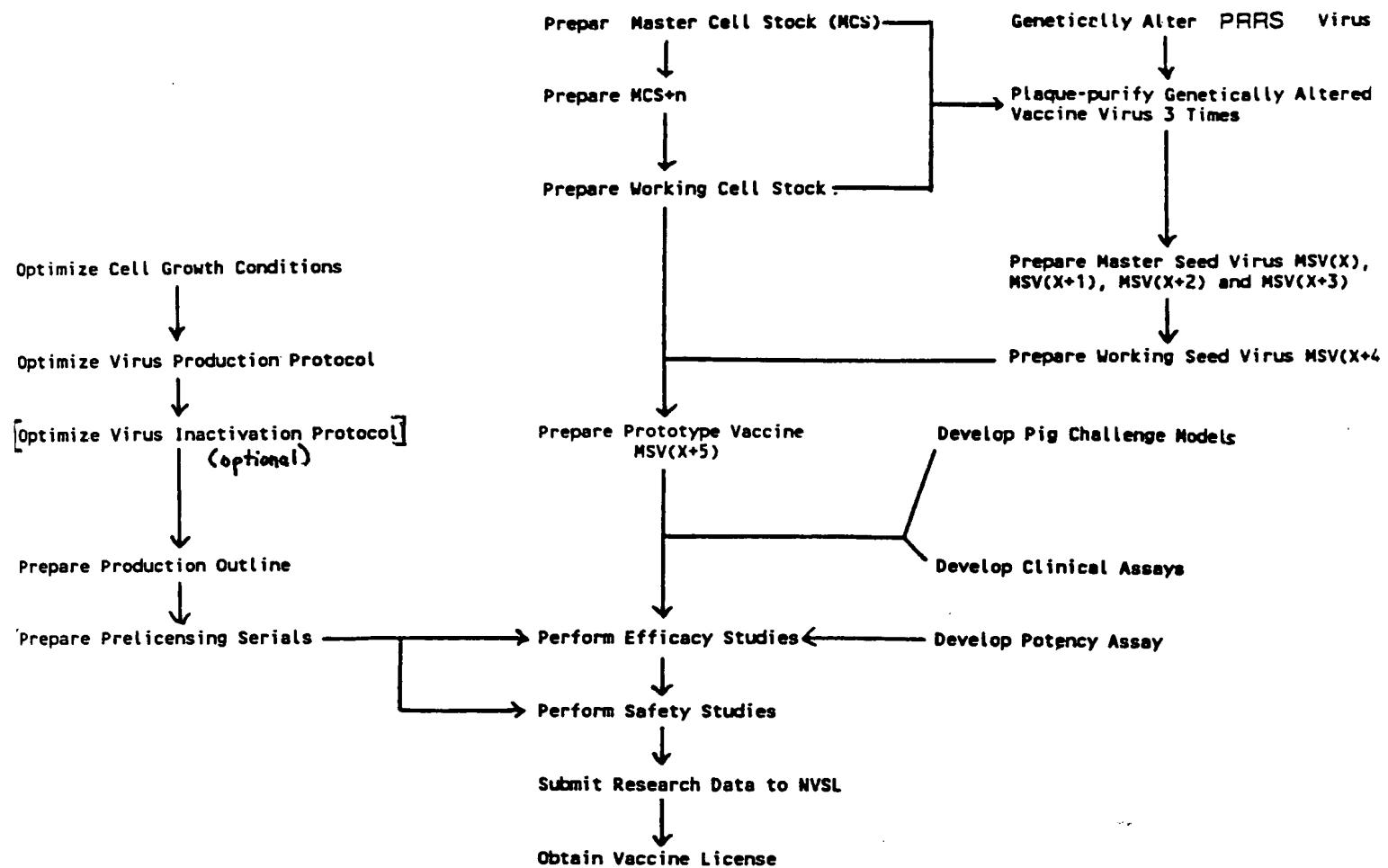


FIGURE 2

ISU-12 cDNA λ Library Construction

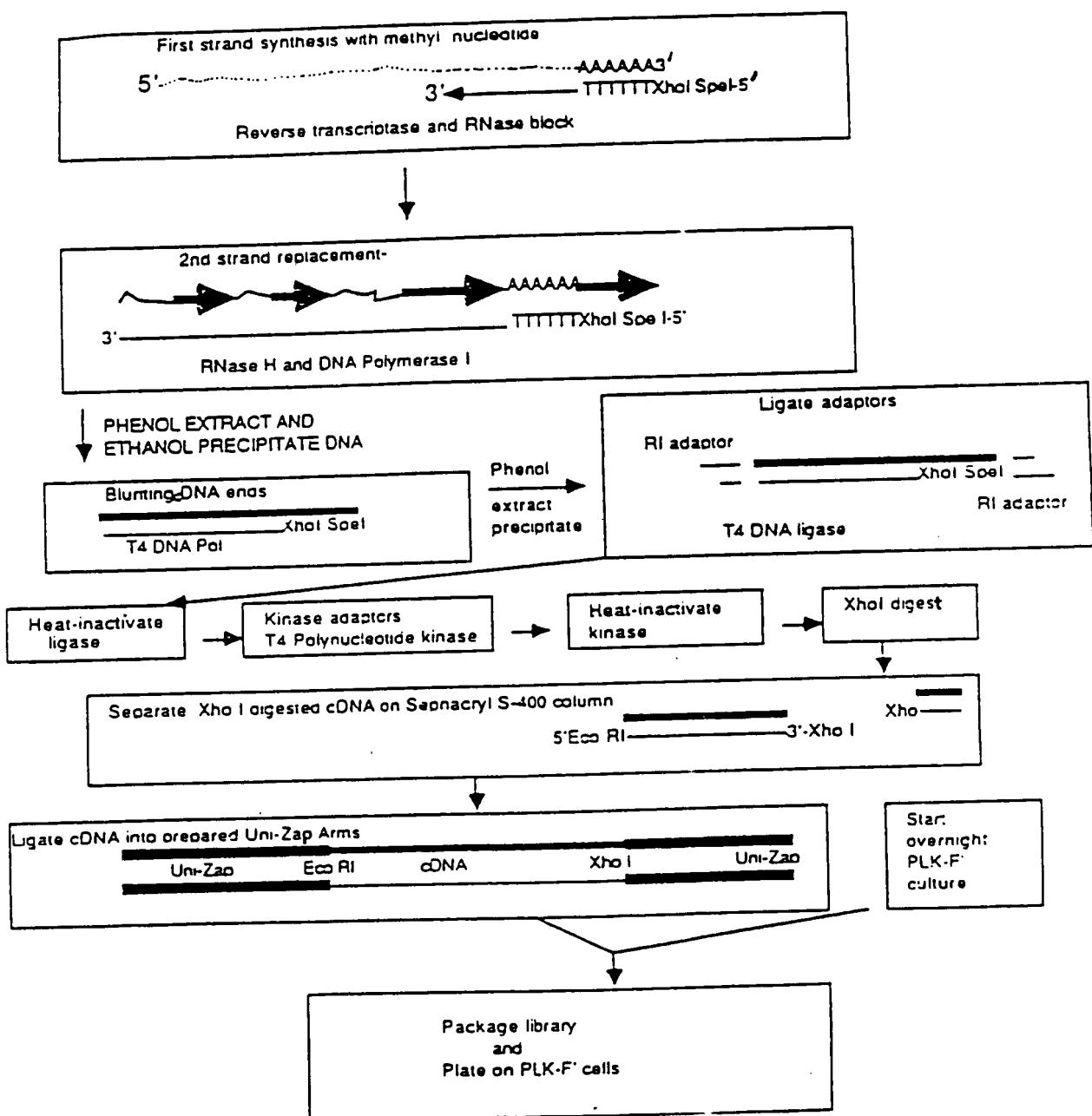


FIGURE 3

Identification of ISU-12 Authentic Clones by Differential Hybridization

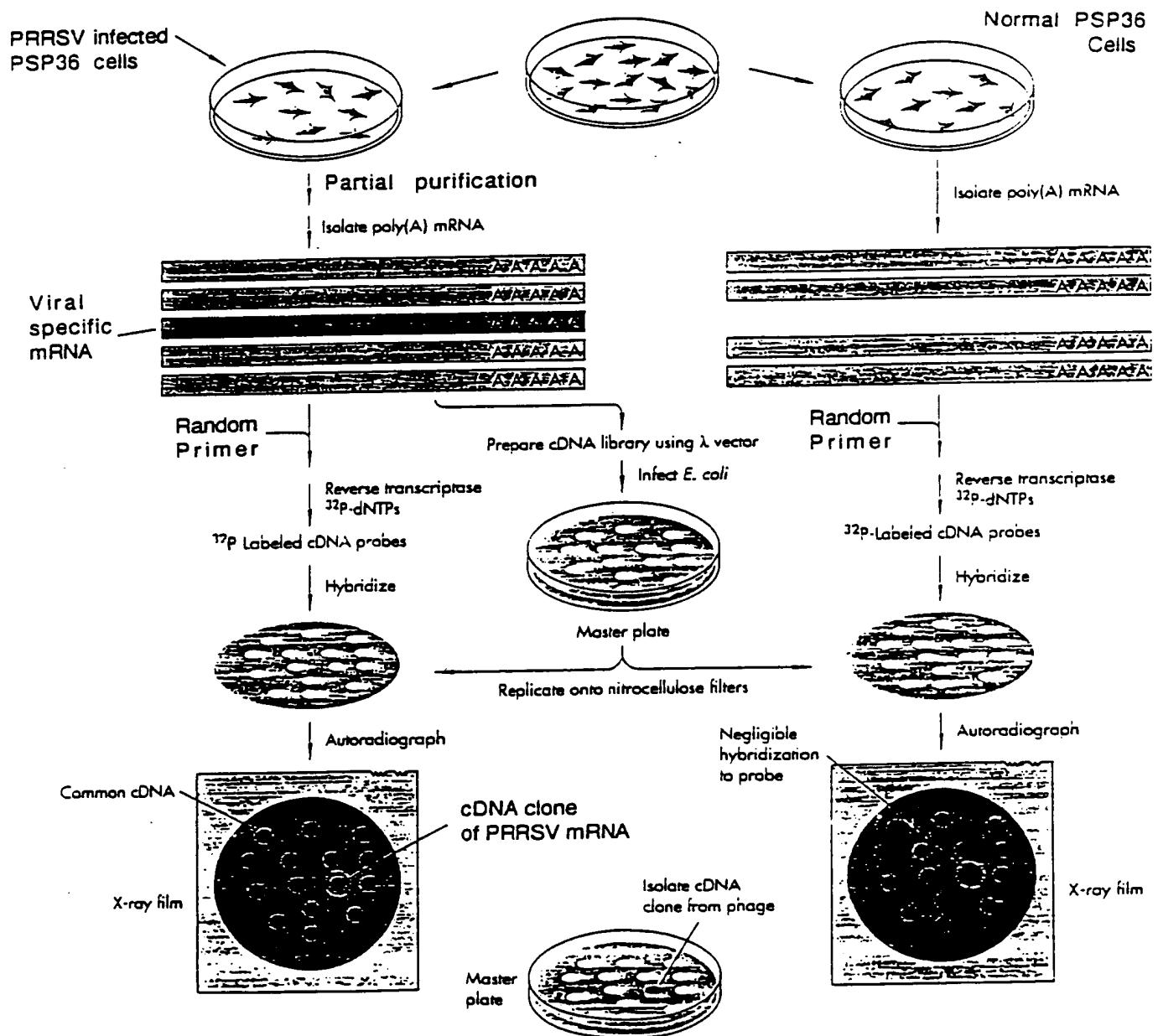


FIGURE 4

1

K_b

9.5—

7.5—

4.4—

2

3

2.4—

4

5

1.4— 6

7

0.24—

FIGURE 5

ISU-12-7a 3' terminal Graphics

FIGURE 6

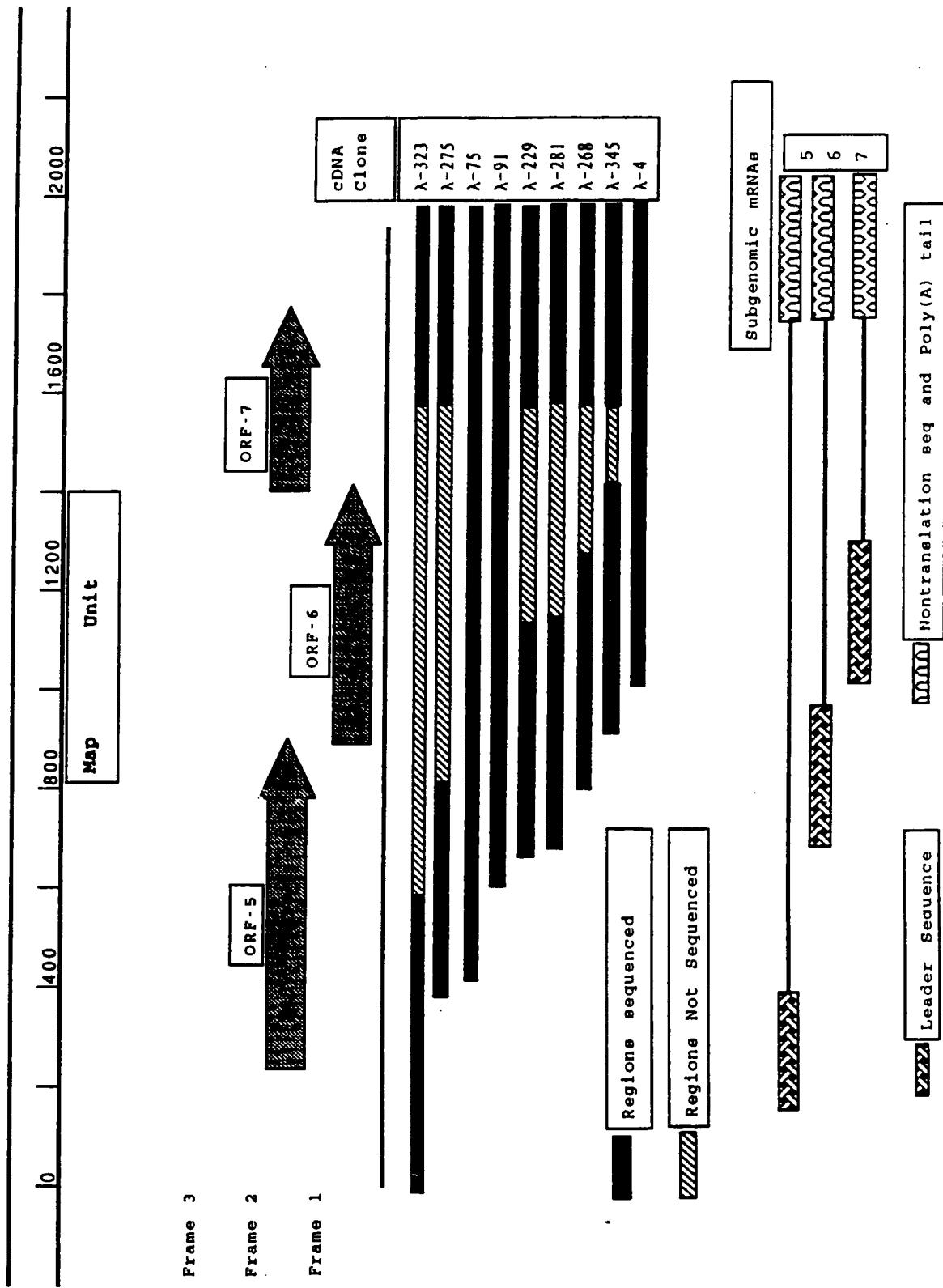


FIGURE 7

GGCAGGCTTGCTGTCCCTCAAAGACATCAGTTGCCCTAGGCATCGCAACTCGGCCCTGAGGGATTGCCAAAGTCCCTCAGTGCACGCCACGGCGATAGGG 100
 ACACCCGTGTATATCACTGTCACAGCCAATGTTACCGATGAGAATTATTTGCAATTCCCTCTGATCTTCTCAAGCTTTCTTCAGCTTCTATGCTTCTG 200
 AGATGAGTAAAAGGGATTAAAGGTGGTATTGGCAATGTTGCAAGGATCTGGCAGTGTGCGTCAACTTACCCAGTTACCTCAACATGTCAGGAATT 300
 TACCCAAACGTTCCCTGGTAGTTGACCATGTCGGCTGCTCCATTTCATGACGCCAGACCATGAGGTGGCAACTGTTTAGCCTGCTTTGGCATT 400
 ORF4 stop *** +1>ORF5 start
 CTGTTGGCAATTTGATGTTAACTATGTTGGGAAATGCTTGACCCGGCTGTTGCTGCCATTGCTTTTTGTTGCTGTTATCGTCCCTTGT 500
 GTTGCCTCGTCAGGCCAACGGAACAGCGGCTCAAATTACAGCTGATTACAACATTGACGCTATGTGAGCTGAATGGCACAGATTGGCTAGCTAATA 600
 AATTGACTGGCACTGGAGTGTTGTCATTTCCTGTTGACTCACATTGCTCTTATGGTCCCTCACTACTAGCCATTTCCTTGACACAGTCGG 700
 TTGTTGTCACTGTGTCACCGCTGGGTTGTTACGGGGTATGTTCTGAGTAGCATGTACCGGTCTGTGCCCTGGCTGCCATTGCTTCGTCAATT 800
 AGGCTTGGAAAGAATTGCATGTCCTGGCCTACTCATGTACCAAGATAACCAACTTCTTGACACTAAGGGCAGACTCTATCGTTGGGGTCCCTG 900
 TCATCATAGAGAAAAGGGCAAAGTTGAGGTGCAAGGTACCTGATGACCTCAAAGAGTTGCTTGATGGTCCGGGTACCCCTGTAACCAGAGT 1000
 ORF6 start +1> ***ORF5 stop
 TTCAGGCCAACATGAGTGTGCTTATGATGACTTCCTGTCATGATAGCACCGTCCACAAAGGTGCTTGGCTTCTATTACCTACAGCCAGTGA 1100
 TGATATATGCCCTAAAGTGTAGTCGGCCGACTGCTAGGGCTCTGACCTTTGGCTTCTCTGAATTGCTTTCACCTTGGGTACATGACATTG 1200
 GCACTTTAGAGTACAAATAAGGTCGGCTCACTATGGGAGCAGTAGTGTGACTCCCTTGGGGGTGACTCAGCCATAGAAACCTGAAATTCA 1300
 TCCAGATGCCCTTGCTTGTCTAGGCCAACGTACATTCTGGCCCTGCCACACGTTGAAAGTGGCAGGGTTTCACTGGATTGGCAAATGATA 1400
 ACCACGGATTTTGTCCGGCGTCCGGCTCACTACGGTCAACGGCACATTGGTCCGGTTAAAAGCCTCGTGTGGGGCAGAAAAGCTGTTAA 1500
 ORF7 start +1> ***ORF6 stop
 ACAGGGAGTGGTAAACCTTGTAAATATGCCAAATAAACCGCAAGCAGAGAAGAGAAAAGGGGATGGCAGCCAGTCAATGCTGTGCCAGAT 1600
 GCTGGTAAGATCATCGTCACCAAAACAGTCAGAGGCAAGGACGGAAAGAAAAATAAGAAGAAAACCGGAGAAGCCCCATTCCCTAGCG 1700
 ACTGAAGATGATGTCAGACATCACTTACCCCTAGTGAGCGTCAATTGTGCTGTCGTCATCCAGACCGCTTTAATCAAGGCCTGGACTTGCACCC 1800
 TGTCAGATTCAAGGAGGATAAGTTACCTGTGGAGTTAGTTGCTACGCACTGTCGCTGATCCGGTCAACAGCATCAGCATG 1900
 GCGCTGGCATTTGAGGCATCCCAAGTGTGAATTGGAAGAATGCGTGGTGAATGGACTGATTGACATTGCTTAAGTCACCTATTCAATTAGGC 2000
 GACCGTGTGGGGTAAGATTAAATTGGCGAGAACACACGGCGAAATTAAAAAAAAAAAAA 2062

Lelystad beg (13484-14089)
ISU-12-3' terminal (426-1028)

Lelystad seq (13484-14089)
ISU-12-3' terminal (426-1028)

ISU-12-3' terminal (426-1028)

Lelystad 869 (13484-14089)
ISU-12-3' terminal (426-1028)

102
ACAAATGGAGCTACCTTGTAG

FIGURE 8

| | | |
|---|---|---------------|
| ISU 12/7a/3' terminal (888 - 1413) Leystad seq (14077 - 14598) | AATGGAGTGG TCCATTAGATG ACCTTGTTGCA TGATAGGAGC GCTTCCAAA AGCTGCTTC -ATGG-GAGG -CTTAGACG ATTTTGCCTA CGATCCATTC GCCGACAAA AGCTGCTTC | 947 14132 |
| ISU 12/7a/3' terminal (888 - 1413) Leystad seq (14077 - 14598) | CGCGTTTCTT ATTACCTACA CGCCAGTGTAT GATAATGCC CTAAGCTGA GTCGGCCCC ACCCTTACG ATCACATACA CACCTTAAT GATAAGCC CTTAACGTGT CACCGGCCC | 1007 14192 |
| ISU 12/7a/3' terminal (888 - 1413) Leystad seq (14077 - 14598) | ACTGGCTAGGG CTGTGGACC TTTCGGCTT CCTGAAATCT CCTTGACCT TCGGTACAT ACTCCCTGGG CTGTGGACA TCCCTAAATT TCTGAACCTG TCTTACAT TCGGATACAT | 1067 14252 |
| ISU 12/7a/3' terminal (888 - 1413) Leystad seq (14077 - 14598) | GACATTCCTG CATTTCAGA GTCACAAATAA GTTCGGCTC ACTATCCGAC CACTACTTC GACATTCCTG CATTTCAT CCACCAACCG TCTGGACCT ACCCTGGG CTGTCGCG | 1127 14311 |
| ISU 12/7a/3' terminal (888 - 1413) Leystad seq (14077 - 14598) | ACTCCCTTGG GGGGTGACT CAGG-CATA GAAACCTGGA ATTATCAC CTCACAGTC -GGCTCTGT GGGCTCTTA CAGCTTCACA GAGTCATGGA AGTATCAC TTCCAGATGC | 1185 14370 |
| ISU 12/7a/3' terminal (888 - 1413) Leystad seq (14077 - 14598) | CGTTTCTGCTT TGGTACGGCG CAAGTACATT TGGCCCCCTG CCCACCACT TGAAGTGCC AGATTCGTT GGGTGGCCG GGGATACATT TGGCCCCCTG CCCACCACT AGAAAGTGCT | 1245 14430 |
| ISU 12/7a/3' terminal (888 - 1413) Leystad seq (14077 - 14598) | CCAGGCTTCTT ATCCATTGCG CCCAAATGAT ACCACCCAT TTTGCTTCCG GCG TCCCGC GCAGGCTCTC ATTCAATCTC AGGTGCGT AACGAGCAT ACCCTTGAG AAAGCCGGGA | 1305 14490 |
| ISU 12/7a/3' terminal (888 - 1413) Leystad seq (14077 - 14598) | TCCACTAAGG TCAACGGCAC ATGGTCCC GGGTTAAAAA GCCTCTGT GGGGGC CTAACATCAG TGAAACGGCAC TCTAGTACCA GGACCTGGGA GCCCTCTGCT GGGGGCAA | 1365 14550 |
| ISU 12/7a/3' terminal (888 - 1413) Leystad seq (14077 - 14598) | AAAGCTGTTT AACAGGGAGT GGTAACCTT GTAAATATG CCAAATAA CGAGCTGTTT AAGGAGGACT GTTAACCTT GGTAAACCTC CTCAACTATG CGCGCTAA | 1413 14598 |

FIGURE 9

Lelystad seq (14588 - 14974)
 ISU 12/70/3' terminal (1403 - 1774) ATGCCCGTAA AAACCCAGA GGCGAAAGGA AAAGAAAAAGT A-CAG---C 14632
 ----- ----- ----- AT CCCAAAATAC ACGGCAAGG AGCAAGAG 1434

Lelystad seq (14588 - 14974)
 ISU 12/70/3' terminal (1403 - 1774) TCGATGGGG AAATGCCAGC CAGTCATACTA ACTGTGCCAG TTGCCGTC 14681
 AAAGAAGGG GATGCCAGC CAGTCATACTA GCTGTGCCAG ATGCCGTC 1483

Lelystad seq (14588 - 14974)
 ISU 12/70/3' terminal (1403 - 1774) CAATGATAAA GTCGCAAGCC CAAGCAACCTA GCGG---A GG ACGGCCAAA 14728
 -AA-GATCAAT CCGTCACAA AAACCACTCA GACCGAAGG ACGGG...GA 1528

Lelystad seq (14588 - 14974)
 ISU 12/70/3' terminal (1403 - 1774) AAGAAAAA-----CCTGACAAG CCACATTTC ACCTCTGC 14766
 AAGAAAAATA AGAAGAAAAA CCCGGACAAG CCCGATTTC CTCTCTGC 1578

Lelystad seq (14588 - 14974)
 ISU 12/70/3' terminal (1403 - 1774) TGAAGATGAC ATCCGGACC ACCTCACCA GACTGAACCP TCCTCTGC 14816
 TGAAGATGAT GTCAGACATC ACCTTACCC TAGTAGGTT CAATTCTGC 1628

Lelystad seq (14588 - 14974)
 ISU 12/70/3' terminal (1403 - 1774) TGCAATTGAT CCAGAAGCT TTCGATCAAG CCCGAGGAAC TCCTCTGC 14865
 TGTCGTCAT CCAGAAGCC TTCGATCAAG CCCGAGGAAC TGGAC-C 1677

Lelystad seq (14588 - 14974)
 ISU 12/70/3' terminal (1403 - 1774) TTTCATCCACC GGCAAGGTC CTTTTCAGT TGAGTTATG CTCCCGTTG 14915
 GTCAATTCA GGGAGGATAA GTTCACACTG GGAGTTACT TTCCTAACCC 1727

Lelystad seq (14588 - 14974)
 ISU 12/70/3' terminal (1403 - 1774) CTCAATTGCT GGCCCTGATT CCCGCTGACTT CTACATCCC CAGTCAGGCT 14965
 ATCAATTGCT GGCCCTGATC CCCGCTCACAG CTACACCC-T CAG-CATCA- 1774

Lelystad seq (14588 - 14974)
 ISU 12/70/3' terminal (1403 - 1774) GCAAGTTAA 14974
 ----- 1774

FIGURE 10

| | | | | |
|--|---|----------------|----------------|---------------|
| ISU 12/7a/3' terminal (1775 - 1938) Leystad seq (14975 - 15101) | ----- ----- | ----- ----- | ----- ----- | 1814 14976 |
| ISU 12/7a/3' terminal (1775 - 1938) Leystad seq (14975 - 15101) | AGAA <u>TGCGTC</u> GTGAATGCCA C <u>TGATTGACA</u> <u>TTCGCGCTCT</u> TGACAGTCAG GTGAATGCC GCGATTGCC <u>TCTCGCCCTCT</u> | 1854 15016 | | |
| ISU 12/7a/3' terminal (1775 - 1938) Leystad seq (14975 - 15101) | A <u>CTCACCTA</u> T <u>TCATTAGG</u> G <u>CGAAGCTGT</u> G <u>GGCCCTAAC</u> G <u>ACTCACCTA</u> T <u>TCATTAGG</u> G <u>CGAAGCTGT</u> G <u>GGCCCTAAC</u> | 1800 15056 | | |
| ISU 12/7a/3' terminal (1775 - 1938) Leystad seq (14975 - 15101) | T <u>TTAAATTGG</u> G <u>AGAACAC</u> A <u>CCGCCAAA</u> T <u>AAAAAAA</u> G <u>TTAAATTGG</u> G <u>AGAACAC</u> A <u>CCGCCAAA</u> T <u>AAAAAAA</u> | 1933 15096 | | |
| ISU 12/7a/3' terminal (1775 - 1938) Leystad seq (14975 - 15101) | <u>AAAAAA</u> <u>AAAAAA</u> | 1938 15101 | | |

FIGURE 11

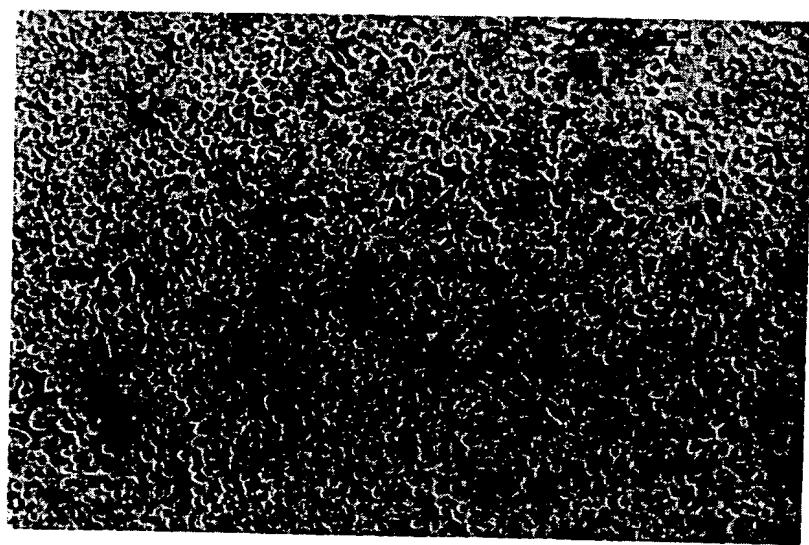


FIGURE 12

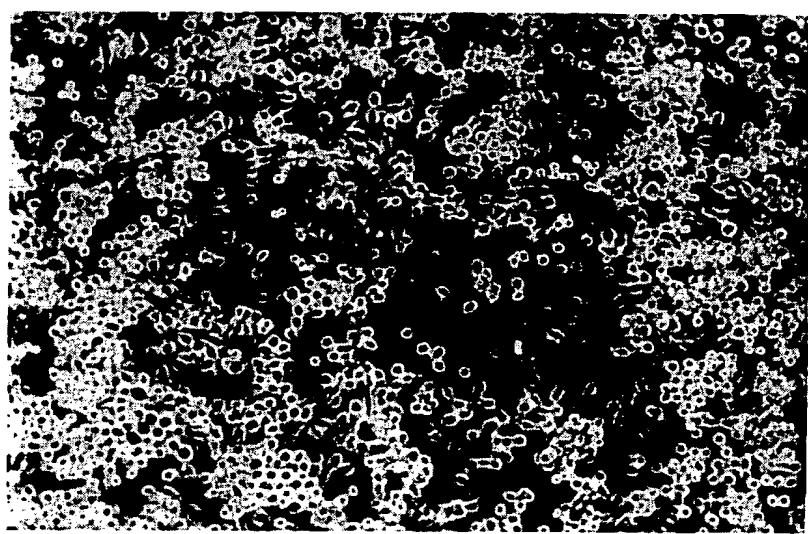


FIGURE 13

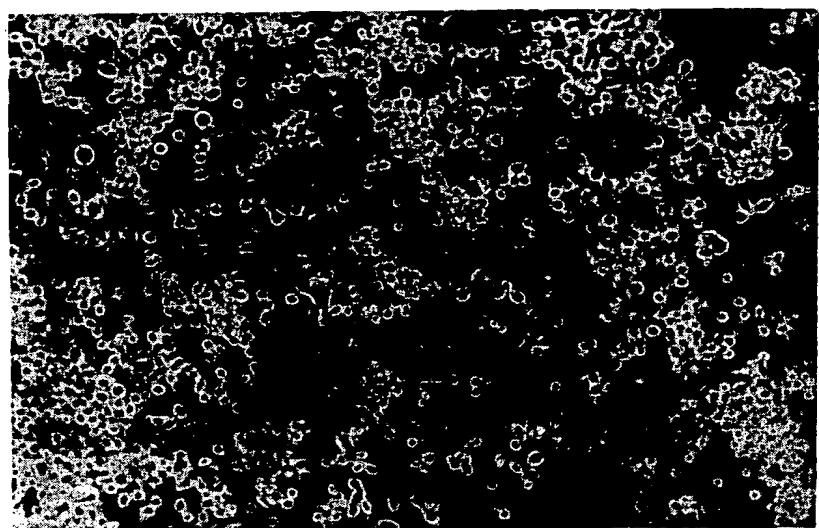


FIGURE 14

SM E M NP E+M+NP SM



FIGURE 15

SM pVL1393 E M NP SM

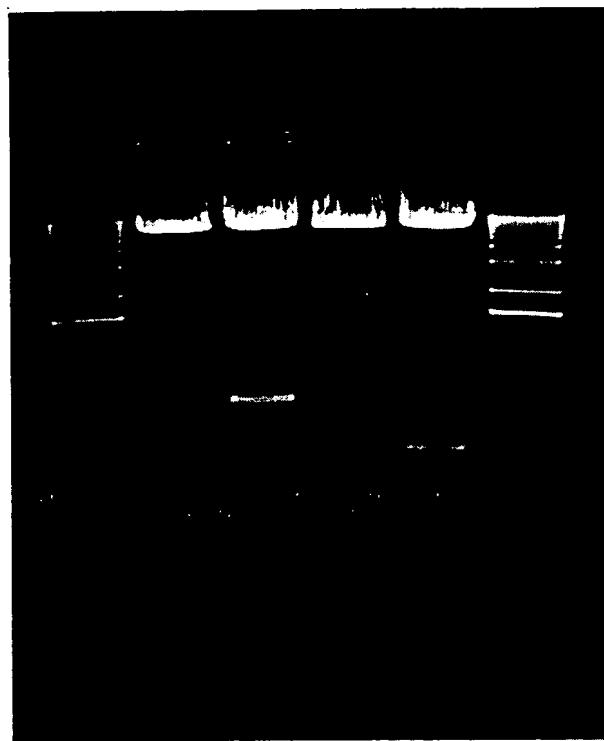


FIGURE 16

FIGURE 17

A

| | | |
|---------------|--|-----|
| VR 2385 ORF6 | MESSLDDFCHDSTAPQKVLLAFSITYTPVMYALKVSRGRLLCLLHLLFLNCAFTPGYMTFVHFQSTNKVALTMGAVVALLWGVYSAIETWKFITSRCR | 100 |
| ISU-1894 ORF6 | .G..... | 100 |
| ISU-22 ORF6 | .G..... | 100 |
| ISU-55 ORF6 | .G..... | 100 |
| ISU-79 ORF6 | .G.....Y..... | 100 |
| ISU-3927 ORF6 | .G.....N..... | 100 |
| LV ORF6 | .G-G.....N.PI.A..LV.....I.....I.I.....S.....Y.....R.....L.....FT.S..... | 99 |
| PRRSV-10 ORF6 | .G-G.....N.PI.A..LV.....I.....I.I.....S.....Y.....R.....L.....FT.S..... | 99 |
| LDV-C ORF2 | .G-G.-E..DQTSWY.-IFI..L..IA..S..F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..TI..SL..I..V..I..TLVKIVDWLVI.. | 96 |
| LDV-P ORF2 | .G-G.-E..DQTSWY.-I..L..IA..S..F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..T..SL..I..V..I..TLVKIVNNMVL.. | 96 |

| | | |
|---------------|---|-----|
| VR 2385 ORF6 | LCLLGRKYI LAPAHHVESAGFHPIAANDNH-----AFVVRPGSTTVNGTLVPGKSLVLGGRKAVKQGVNLVKY-AK | 183 |
| ISU-1894 ORF6 | | 174 |
| ISU-22 ORF6 | | 174 |
| ISU-55 ORF6 | | 174 |
| ISU-79 ORF6 | | 174 |
| ISU-3927 ORF6 | | 174 |
| LV ORF6 | .C..R.....L.S.S.SG.R.....YA..K..L.S.....R.....KR..R.....-GR | 173 |
| PRRSV-10 ORF6 | .C..R.....L.S.S.SG.R.....YA..K..L.S.....R.....KR..R.....-GR | 173 |
| LDV-C ORF2 | .P..S..PS..D-----TSDGRQSLTTSLTT..K..L..Q..DPQR..K..SK.A..L..VS. | 171 |
| LDV-P ORF2 | .F..S..PS..D-----TSDGRQSLTTSSTT..K..L..Q..DPQR..K..SK.A..L..VS. | 171 |

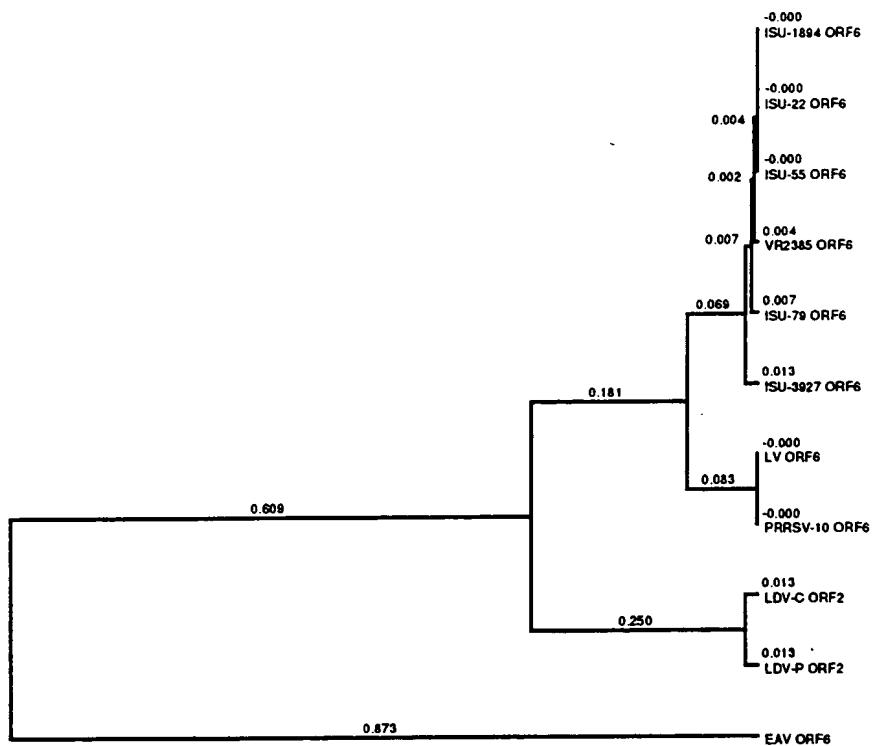
B

| | | |
|---------------|--|-----|
| VR 2385 ORF7 | MPNNNTGKQQKRKK-----GDGQPVNOLCQMLGKIIAHQNQSRGKPGKKNKKKNPEKPHFPLATEDDVRHHPTPSERQLCLSSIQTAFNQGAGTCTLS | 100 |
| ISU-1894 ORF7 | ...N..... | 93 |
| ISU-22 ORF7 | ...N..... | 93 |
| ISU-79 ORF7 | ...N..... | 93 |
| ISU-3927 ORF7 | ...N.....K..... | 93 |
| ISU-55 ORF7 | ...N.....K..... | 93 |
| VR2332 ORF7 | ...N.....TEE..... | 93 |
| LV ORF7 | ---A..N.SQ..KKSTAPM.N.....L..AM.KS.R---QPR.GQA..K.....A..I..L.QT..S..Q.....AS.. | 94 |
| PRRSV-10 ORF7 | ---A..N.SQ..KKSTAPM.N.....L..AM.KS.R---QPR.GQA..K.....A..I..L.QT..S..Q.....PS.. | 94 |
| LDV-C ORF1 | ..SQ..KK..GGQN.....AN.....N.LISALLRNAG..--N..K.Q.K..-Q..-L..M..GPS..L..VM..N.V.M.R..LV..L..G.Q..V | 85 |
| LDV-P ORF1 | ..SQ..KK..SGQN.....AN.....N.LINALLRNAG..--N..K.Q.K..-Q..-L..M..GPS..L..VM..N.V.M.R..LV..L..G.Q..V | 85 |
| EAV ORF7 | .ASRRSRP..AASF-----RN.R--RRQPTSYNDLLRMPG-----MRVR..PPAQPTQAI..EPG..L..DLNQQ..ATLS..NV..RF..MI..H..SL..-A | 83 |

| | | |
|---------------|------------------------------------|-----|
| VR 2385 ORF7 | DSGRISYTVEFSLPTHHHTVRLIRVTASP---SA | 134 |
| ISU-1894 ORF7 | | 123 |
| ISU-22 ORF7 | | 123 |
| ISU-79 ORF7 | | 123 |
| ISU-3927 ORF7 |P..... | 123 |
| ISU-55 ORF7 | | 123 |
| VR2332 ORF7 | | 123 |
| LV ORF7 | S..KV..FQ..M..VA.....STSASQGAS | 128 |
| PRRSV-10 ORF7 | S..KV..FQ..M..VA.....STSASQGAS | 128 |
| LDV-C ORF1 | ...G.NF..S.M....A.....NAS.NS----- | 115 |
| LDV-P ORF1 | ...G.NF..S.M....A.....NAS.NS----- | 115 |
| EAV ORF7 | .A.GLT...SW-V..KQIQ..KVAPP.G----- | 110 |

FIGURE 18

A



B

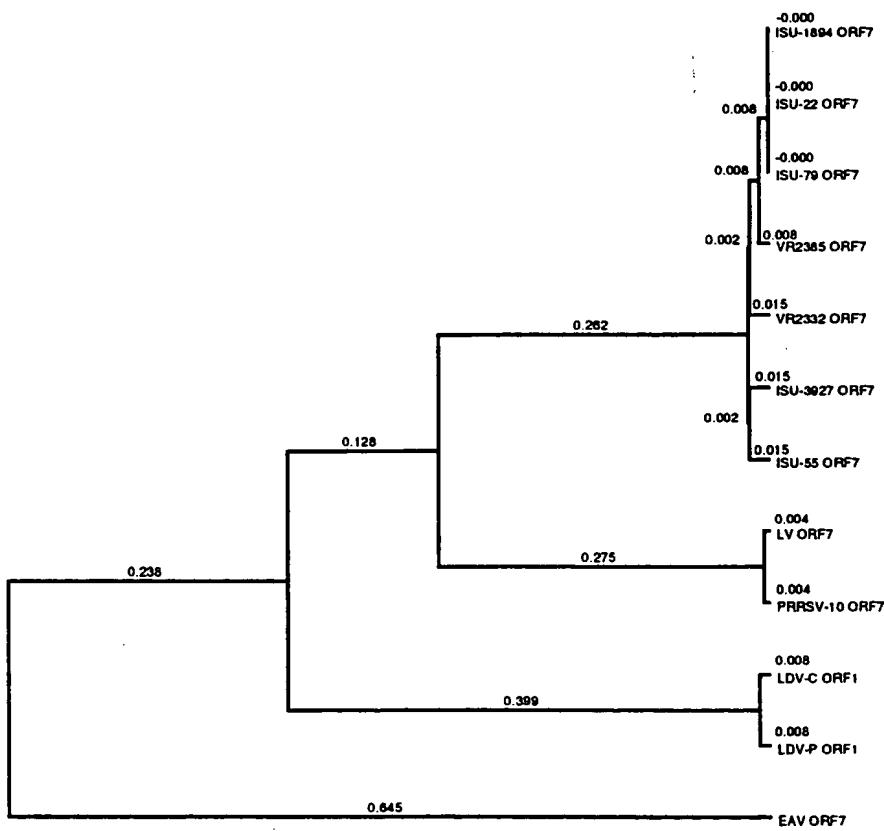


FIGURE 19

+ Start ORF2
 CCTGAATTGAGATGAAATGGGGCTATGCAAAGCCTTTTGACAAAATTGCCAACTTTTGATGCTTCACGGAGTTCTGGTGTCATTGAT 100
 ATCATTATATTTGGCCATTGGCTTCACCATCGCAGGTTGGCTGGTCTTTGATCAGATTGGTTGCTCCGGATACTCCGTGGCGCC 200
 CTGCCATTCACTCTGAGCAATTACAGAAGATCCTATGAGGCCCTTCTCTCAGTGCCAGGTGGACATTGCCACCTGGGAACATAAACATCCTGGGA 300
 TGCTTTGGCACCATAAGGTGTCACCCCTGATGAAATGGTGCGCTCGAATGTACCGCATCATGGAAAAGCAGGACAGGCTGCCCTGAAACAGT 400
 AGTGAGCGAGGCTACGCTGTCGCATTAGTAGTTGGATGTGGTGCTCATTTGAGCATCTTGCGCCATTGAAGCCGAGACCTGAAATATCTGCC 500
 ✓TCTCGGCTGCCCATGCTACACCACCTGCGCATGACAGGGTAAATGTAACCATAGTGATAAATAGTACTTGAATCAGGTGTTGCTTTGCCAACCC
 + Start ORF3
 CTGGTCCCGGCAAAGCTCATGATTCCAGCAATGGCTAAATGCTGACATTCCCTATATTTCTCTGAGCTTCGACTCTGACTCTTTGCTGCT 700
 GCTGTGGTTCGGGTTCCAATGCTACGTACTGTTGGTTCCGCTGGTAGGGCAATTGCTTGCAGACTACGGTGAATTACACGGTGTGCCCGC 800
 CTTGCGCTACCCGGCAAGCAGCCGAGAGGCTACGAACCCGGCAGGTCCCTGGTGAGGATAGGCATGATGATGTGGGAGGACGATCATGATGA 900
 ACTAGGGTTGTGGTGCCGCTGCCCTCAGCGAAGGCCACTGACCACTGACAGTGGCTTGGCTGGCTCCCTGTCAGCTATACGGCCAGITC 1000
 CATCCCGAGATACTGGGATAGGAATGTGAGTCGAGTCTATGTTGACATCAAGCAGCAATTCACTTGGCTGTTGATGGCAGAACACCACTTGC 1100
 CCCACCATGACAACATTTCAGCCGTGCTCAGACCTATTACCAAGCATCAGTCGACGGGGCAATTGGTTACCTAGAATGGGTGCTCCCTTTC 1200
 CTCTTGGTTGGTTAAATGCTCTTGGTTCTCAGGCCTGCCCTGCAAGCCATGTTGAGTCGAGTCTTCAGACATCAAGACCAACACCCAG 1300
 CGGCAGGCTTGTGCTCTCCAAGACATCAGTTGCCCTAGGCATCGCAACTCGGCTCTGAGGGGATTGCAAAGTCCCTGAGTGGCCACGGGATAGG 1400
 GACACCCGTATATCACTGTCACGCCATGTTACCGATGAGAATTATTCGATTCCTCTGATCTCTCATGCTTCTCTGCTTTCTATGCTTCT 1500
 GAGATGAGTGAAAGGATTAAAGGTGGATTGGCAATGTGTCAGGCATGTCGGAGTGTGCTCAACTTACCAAGTTACGTCACATGTCAGGAAT 1600
 TTACCCAACGTTCCCTGGTAGTTGACCATGTCGGCTGCCATTGATGACGCCGAGACCATGAGGTGGCAACTTGTGCTGCTTTTACCAT 1700
 ***Stop ORF4 +Start ORF5
 TCTGTTGGCAATTGAAATGTTAAACTGTTGGGAAATGCTTGACCCGGGCTGTTGCTCCAAATTGCTTTTTATGGTGTATCGTGCCCTTGGTT 1799

FIGURE 20

FIGURE 21

A

| | | |
|--------------|--|-----|
| Consensus | M.WG.C..K.....L....W.....L..SL...P..CL.SPSQ.G.WSF.S.WFAPR.SVRALPFTL.NYRRSYE..L..C..D.P....KH | 100 |
| LV ORF2. | .Q..H.GV.SASCWTTPS.SSLLV.LI-----PF...Y..G....D.Y...F.E....F.....P.....GL.PN.RP.V.QFAV.. | 90 |
| VR2385 ORF2. | .K.L.----AFLTK.AN-FL.MLSRSSWCP.LI..YFW.F..A....V.W...A.D....Y.....S.....AF.SQ.QV.I.TWGT.. | 93 |
| Consensus | PLGM.WH..VS.LIDEMVSRR.Y..ME..GQAAWKQVV.EATL..S.LD.V.HFQHLAA.EA..C..L.SRL.ML..L.....NV..YN.TL..V... | 200 |
| LV ORF2. |F..MR..H.....I.QT..HS.....G...TKL.G..I.T.....V..DS.RF.S...V..KN.AV--G..SLO..T..DR.ELI | 188 |
| VR2385 ORF2. |L..HK..T.....M.RI..KA.....S...SRI.S..V.A.....I..ET.KY.A...P..HH.RMTGS..TIV..S..NO.FAV | 193 |
| Consensus | PPTPG.RPKL.DP.QWLI.VH.SIFSSVA.S.TLF.VLWLR.P.LR.VFGF.W..A..... | 264 |
| LV ORF2. |T....T.R....S.A.....S.V....I.....I.A..Y...H.PT.--THHSS | 249 |
| VR2385 ORF2. |S....H..Q....A..S.....A.C..V....V.M..T...R.LG.IFLNSR- | 257 |

B

| | | |
|--------------|---|-----|
| Consensus | MA..C....FLC....Y....A....S..T.CFWFPL..GN.SFELT.NYT.C.PC.T.QAA...EPGR..WC.IGHDRC.E.DHDEL...PSG... | 100 |
| LV ORF3. | ..HQ.ARHFH..GFIC.LVHS.LASN.SS.L.....AH..T.....I..I.M..S.S..RQRL..NM..K.....E.R.....LMSI...YDN | 100 |
| VR2385 ORF3. | ..NS.TFLYI...CSFL.SFCC.VVAG.NA.Y.....VR..F....V..V.P..L.R..AEAY....SL..R.....G.D.....GFVV..LSS | 100 |
| Consensus | ...L...YAWLA.LSFSY.AQFHPE.FGIGNSRV.VD..HQFICA.HDG.N.T.....NISA....YY.HQ.DGGNWFHLEW.RP.FSSWLVLN.SWFL | 200 |
| LV ORF3. | ...L-K.EGY....F....A.....L.....F..KR.....E..H.S.VSTGH...LYAA..H..I.....L..L.....I.... | 199 |
| VR2385 ORF3. | EGH.TSA....S....T.....I.....Y..IK.....V..Q.T.LPHHD...VLQT..Q..V.....V..F.....V.... | 200 |
| Consensus | RRSP.S.VS.R..Q..RPT.P.....S..TS....L.....R.F.....K.S..... | 266 |
| LV ORF3. |V.P..R.IY.IL...R.RLPVSW.FR..IVSD.TGSOORK.K.PSESRRPNV.P.VLPSTSR | 265 |
| VR2385 ORF3. |A.H..V.VF.TS...P.QRQALL.SK..V--A.GIATRPL.R.A-----LSAARR- | 255 |

C

| | | |
|--------------|---|-----|
| Consensus | M.A..LF.L.G....VS.APACKPCFS..LSDI.TNTAAAGF.VLQDI.C.R.....A.E.I..K..QCR.A.GTP.YIT.TANVTDE.YL..DL | 100 |
| LV ORF4. | ..A.AT..F.A.AQHIM..E.....TH...E.....M....N.F.PHGUSA.Q.K.SPG.SS...E.V...Q..I.....S..YNA.. | 100 |
| VR2385 ORF4. | ..G.SL..L.V.FKCLL..Q.....SS...K.....A.....S.L.HR--NS.S.A.R--.VP...T.I....V.....N..HSS.. | 96 |
| Consensus | LMLS.CLFYASEMSEKGFKV.FGNVSG.V..CVNFT.YV.HV...TO...V.....RLLHF.TP..MRWAT..ACLF.ILLAI. | 184 |
| LV ORF4. |A.....I.....V.SA....D..A..TOH..QHHL.IDHI....L..SA....TI....A..... | 183 |
| VR2385 ORF4. |S.....V.....I.AV....S.Q..KEF..RSLV.DH-V....M..ET....VL....T..... | 179 |

FIGURE 22

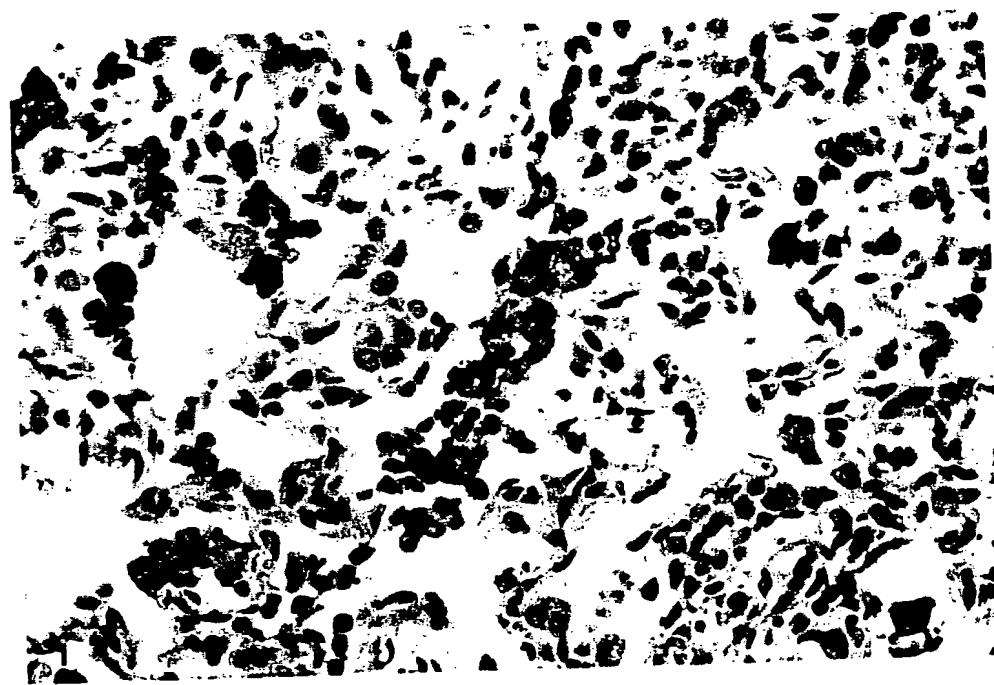


FIGURE 23

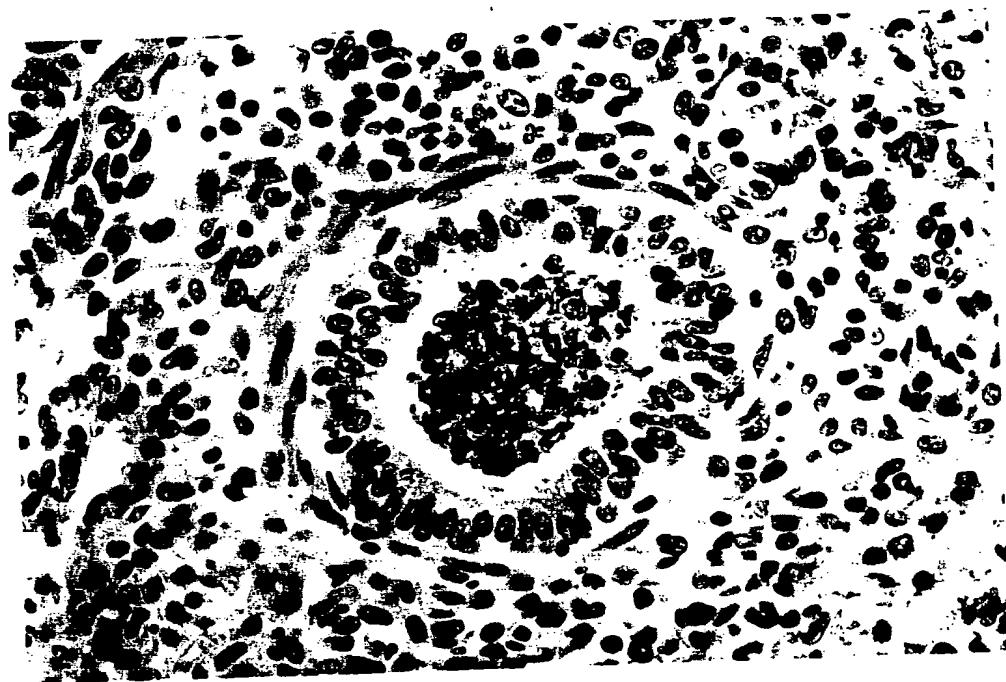


FIGURE 24

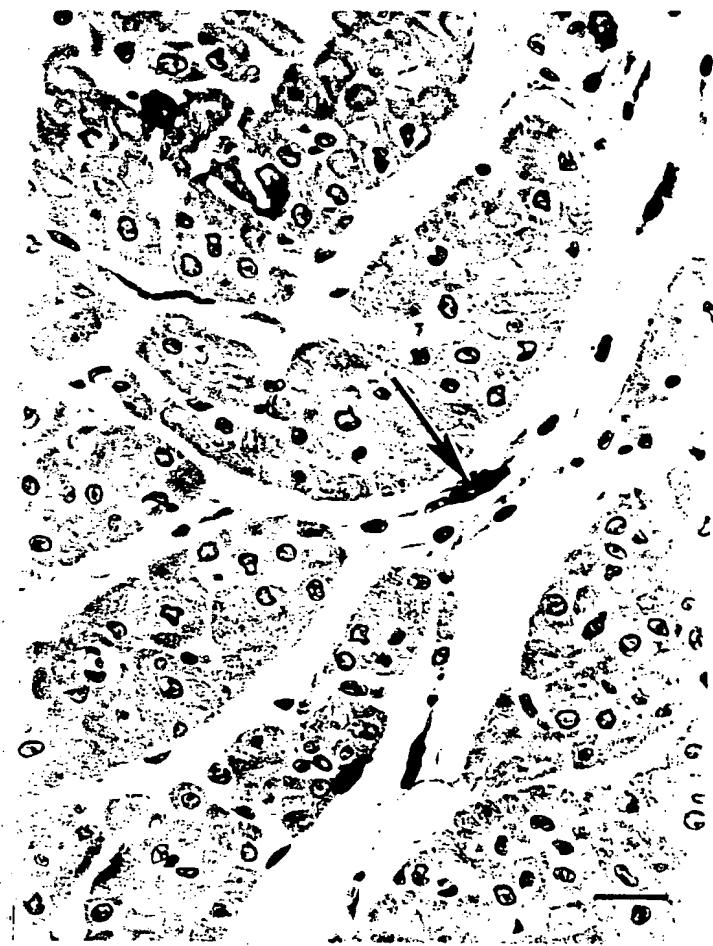


FIGURE 25

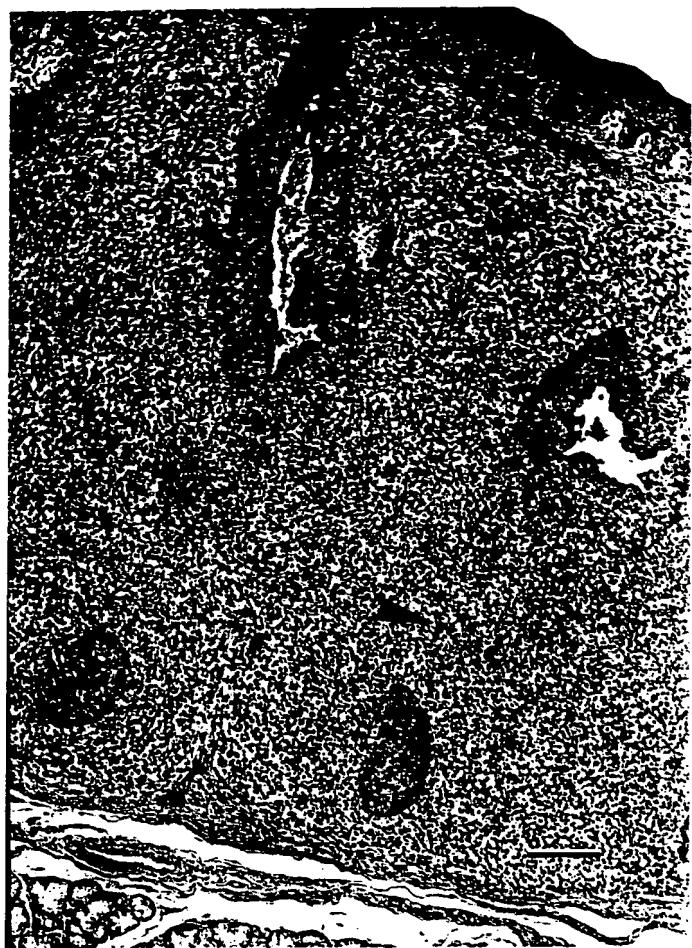


FIGURE 26

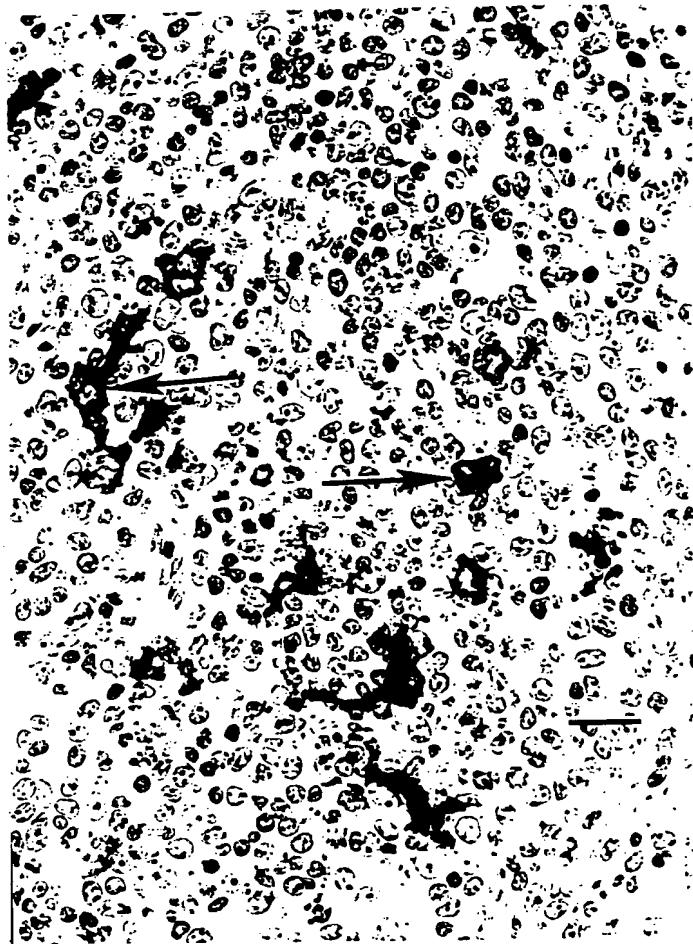


FIGURE 27

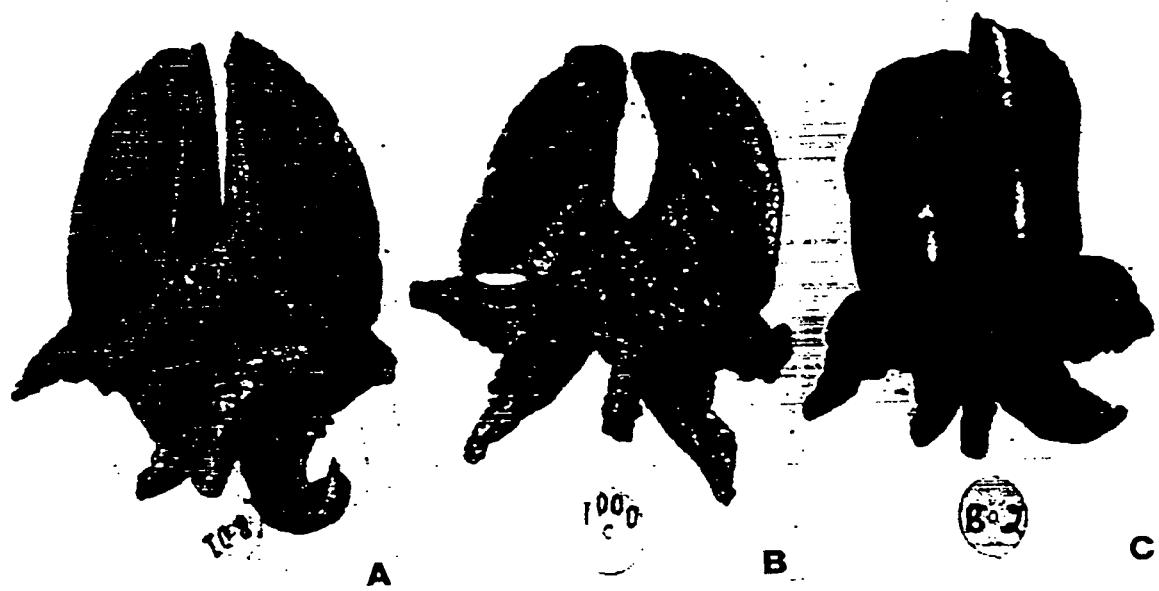


FIGURE 28

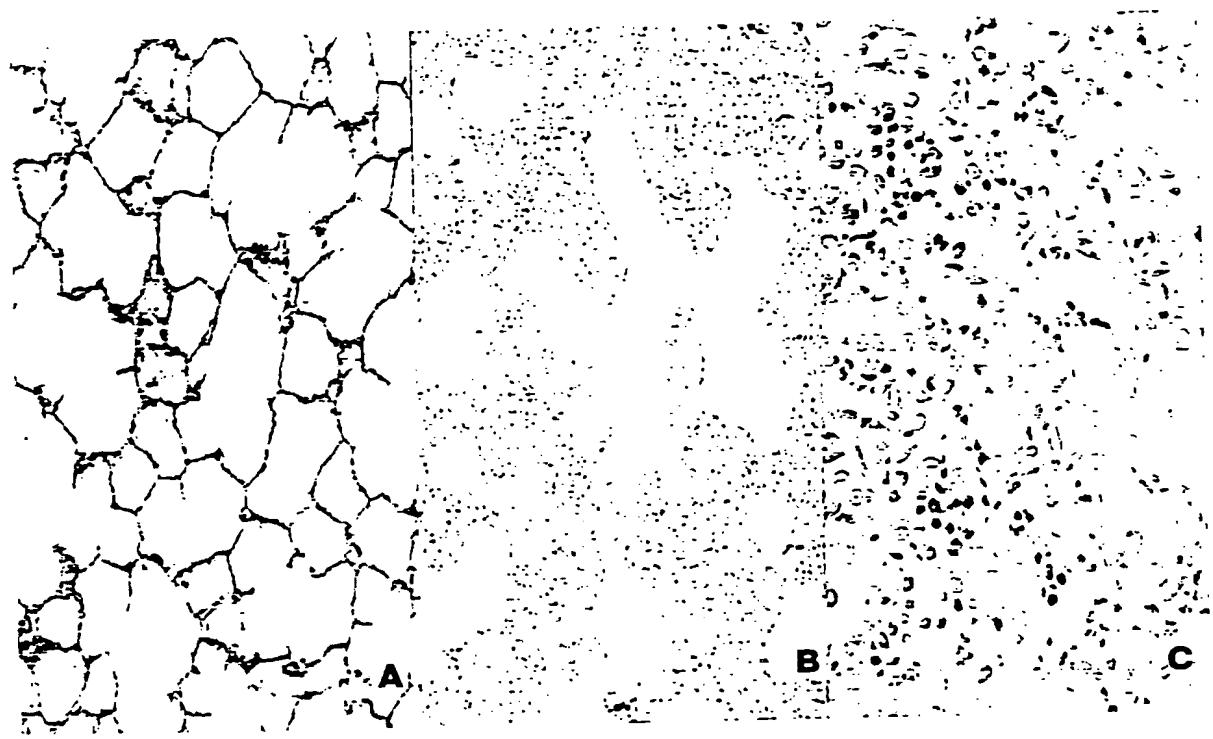
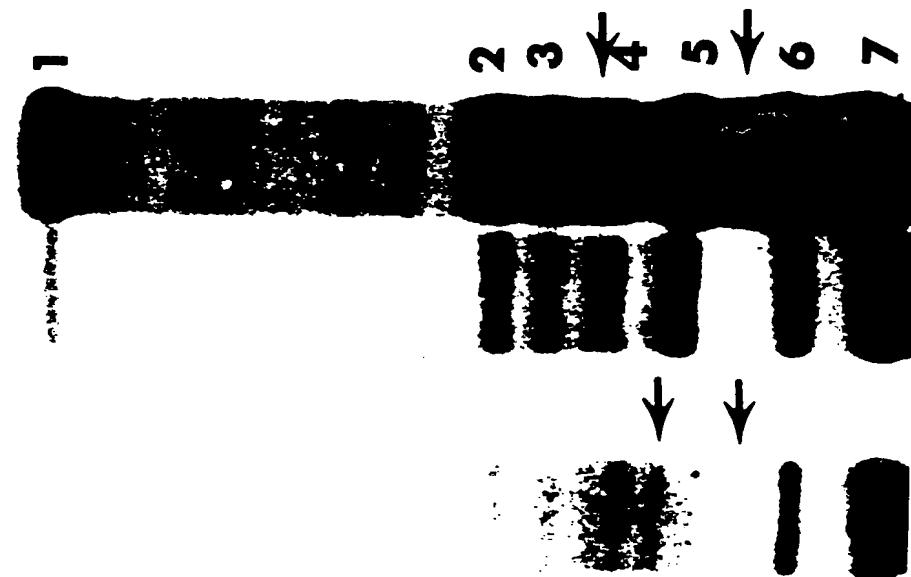


FIGURE 29

1894 3927

22 55 79



A



B

FIGURE 30